Amendments to the Specification:

Please amend the specification pursuant to 37 C.F.R. § 1.121, as follows:

At page 24, please delete paragraph 95 and insert the following replacement paragraph:

--~~(tblastn, http://www .ncbi.nlrn.nih. gov/BLAST/).~~ A novel transcript termed A34 was identified, which upon hypothetical translation showed 31% amino acid identity with A33, including limited conservation of a putative signal sequence, immunoglobulin (1g)-like domains and a transmembrane domain, suggesting it, encoded a cell surface protein. The A34 transcript was represented by Unigene cluster Hs.177164 ~~(http://www .ncbi. nlm.nih.gov/entrez)~~, which contains a full length testisderived cDNA clone, MGC:44287 (Genbank Acc. No. BC043216), as well as 15 other homologous expressed sequence tags (ESTs), derived mainly from normal testis (7 ESTs), and also from normal stomach (2 ESTs), normal aorta (1 EST), uterine cancer (2 ESTs), pancreatic cancer (I EST), and pooled tissues (2 ESTs). The limited distribution of homologous ESTs suggested that the A34 transcript was differentially expressed.—

At page 24, please delete paragraph 96 and insert the following replacement paragraph:

--Analysis of the human genome database ~~(http://www.ncbi.nlm.nih.gov/genome)~~ mapped the gene encoding A34 to chromosome Xq22.1. Thus, A34 shares certain characteristics, such as a prevalence of testis-derived ESTs and mapping to chromosome X, with members of the cancerltestis (CT) antigen family, a group of immunogenic proteins whose expression is restricted to gametogenic tissue and cancer, and are considered target molecules for therapeutic cancer vaccines. Therefore, on the basis of its similarity with the A33 colon cancer antigen, the limited tissue distribution of homologous ESTs, and its similarity with CT antigens,

the A34 gene product became the focus of our search for novel cell surface molecules expressed in cancer.—

At page 26, please delete paragraph 101 and insert the following replacement paragraph:

--The extracellular domain of A34 has 6 potential N-linked glycosylation sites. Given that the average size of an oligosaccharide chain is approximately of 2.5 kDa, the carbohydrate portion of A34 could potentially contribute approximately 15 kDa of mass, and thus the predicted size of native A34 protein (less the signal peptide of 2.3kDa) is 54.4 kDa. Hydrophobicity plots and transmembrane domain prediction software~~:~~

~~http://sosui.proteome.bio.tuat.ac.jp/sosuiframe0.html and~~

~~http://www.cbs.dtu.dk/services/TMHMM/)~~

located a transmembrane domain at residues 234-256, which was followed by a C-terminal intracellular domain encornpasing residues 257-387. The A34 intracellular domain contained 7 sites of potential serine/threonine phosphorylation (casein kinase II phosphorylation sites), and a GSK3 phosphorylation site. Two TRAF2-binding consensus motifs are present at amino acids 314-317 and 324-327. Furthermore, a unique pattern of glutamic acid/proline repeats (EP) is found in the carboxyl terminus of A34. This pattern is found in only two other known human proteins, hematopoietic lineage cell specific protein (HS1) and src substrate protein p85fcortactin.--